

SUBCLASS

FIG. 1

BLASTP - query = 147_TR1; Hit = swiss|O15393|TMS2_HUMAN

This hit is scoring at : 3e-66 (expectation value)

Alignment length (overlap) : 370

Identities : 38 %

Scoring matrix : BLOSUM62 (used to infer consensus pattern)

Database searched : nrdb

Q: 36 CDGVVDCKLKSDELGCVRFDWDKSLKIYSGSSHQWLPICSSNWNDSEKTCQQLGFES
CDGV .C. .DE CVR. . :L::YS.....W P:C::WN::Y....C::G:::
H: 133 CDGVSHCPGGEDENRCVRLYGPNFILQMYSSQRKSWHPVCQDDWNENYGRAACRDMGYKN

AHRTTEVAHRDFANSFSILRYNST IQESLHRSE CPSQRYISLQCSHCGLRA
.:.: D :.S S.:.N.: I.:L:.S: C.S.:.SL:C CG:.. :
NFIYSSQGIVDD SGSTSFMKLNTSAGNVDIYKKLYHSDACSSKAVVSLRCLACGVNLNSS

MTGRIVGGALASDSKWPWQVSLHFGTTHXGGTLIDAQWVLTAAHCCFVTTREKVLEG---
...RIVGG. A ...WPWQVSLH. ...H:CGG::I::W::TAAHC. EK L..
RQSRIVGGESALPGAWPWQVSLHVQNVHVCSSIIITPEWYTAAHCV EKPLNNPWH

TRYPSIN HIS

WKVYAGTSNLHQLPEAAS--IAEIIINSNYTDEEDDYDIALMRLSKETLSGEGICTP
W.:AG. . . : .A. :.:I :.NY..... DIALM:L.KPLT... : :C.P
WTAFAGILRQSFMYGAGYQVQKVISHPNYDSKTKNNDIALMKLQKPLTFNDLVKPVCLP

RSPAPQPQHPLQPSHLASVNSYPGPKASADKTSPFLREVQVNLIDFKKCNDYLVYDSYL
. P LQP..L . :.: G.....KTS..L....V LI: :.CN. .VYD:..
N PGMMLQPEQL-CWISGWGATEEKGKTSEVLNAAKVLLIETQRCNSRYVYDNL

TPRMMCAGDLRGGRDSCQGDSCGGPLVCEQNNRWYLAGVTSWGTGCGQRNKPQVYTKVTEV
TP.M:CAG L:G. DSCQGDSCGGPLV...NN W:L:G TSWG:GC.:. :PGVY .V..
TPAMICAGFLQGNVDSQGDSCGGPLVTSNNNIWWLIGDTSWGSACAKAYRPGVYGNVMVF

TRYPSIN_SER

LPWIYSKMEA 389
..WIY.:M:A
TDWIYRQMA 490

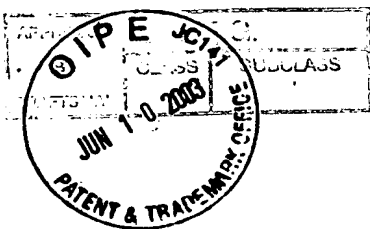


FIG. 2

Prosite search results

PS00134	187->193 TRYPSIN_HIS	PDOC00124
PS00135	334->346 TRYPSIN_SER	PDOC00124

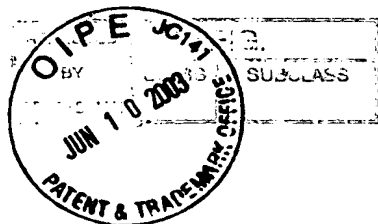


FIG. 3

BLOCKS search results

AC#	Description	Strength	Score
BL00495N	Apple domain proteins.	1945	1582
AA#	325 AGdlrGGrDsCqGDSGGPLVCeqNnRWyLaGvTSW (SEQ ID NO:15)		
BL01253G	Type I fibronectin domain proteins.	1641	1548
AA#	332 rDsCQGDSSGGPLVC (SEQ ID NO:16)		
BL00134A	Serine proteases, trypsin family, histidine p	1500	1524
AA#	175 CGGTLIDaQWVLTAHC (SEQ ID NO:17)		
BL00021D	Kringle domain proteins.	1556	1510
AA#	341 GPLVCEQNNRWYLaGVTSWGtGCGQRNKPGVYTKVTevLPWI (SEQ ID NO:18)		
BL01253H	Type I fibronectin domain proteins.	1765	1508
AA#	351 WYLaGvtSWGtGCGQRNKPGVYTKVTevLpWIysk (SEQ ID NO:19)		
BL00021B	Kringle domain proteins.	1547	1507
AA#	175 CGGTLIDaQWVLTAHC (SEQ ID NO:20)		
BL00495O	Apple domain proteins.	1756	1383
AA#	360 GtGCGQRnkPGVYTKVTevlpWIysKmeA (SEQ ID NO:21)		
BL00134B	Serine proteases, trypsin family, histidine p	1289	1299
AA#	333 DSCQGDSSGGPLVCEqNNRWYLAGV (SEQ ID NO:22)		
BL01209	LDL-receptor class A (LDLRA) domain proteins.	1413	1274
AA#	35 CDGVVDCKlKSDE (SEQ ID NO:23)		
BL01253F	Type I fibronectin domain proteins.	1693	1270
AA#	288 AdktSpFLREvQVnLidfkKCndylVYdSylTPrMmCAG (SEQ ID NO:24)		
BL00495L	Apple domain proteins.	1947	1263
AA#	209 tSnlhqlpeaaSiaEIIInsNYtdeEddyDIALmrLskP (SEQ ID NO:25)		
BL00134C	Serine proteases, trypsin family, histidine p	1245	1254
AA#	369 PGVYTKVTEVLPWI (SEQ ID NO:26)		
BL01253D	Type I fibronectin domain proteins.	1398	1217
AA#	175 CGGtLIdaqWVLTA (SEQ ID NO:27)		

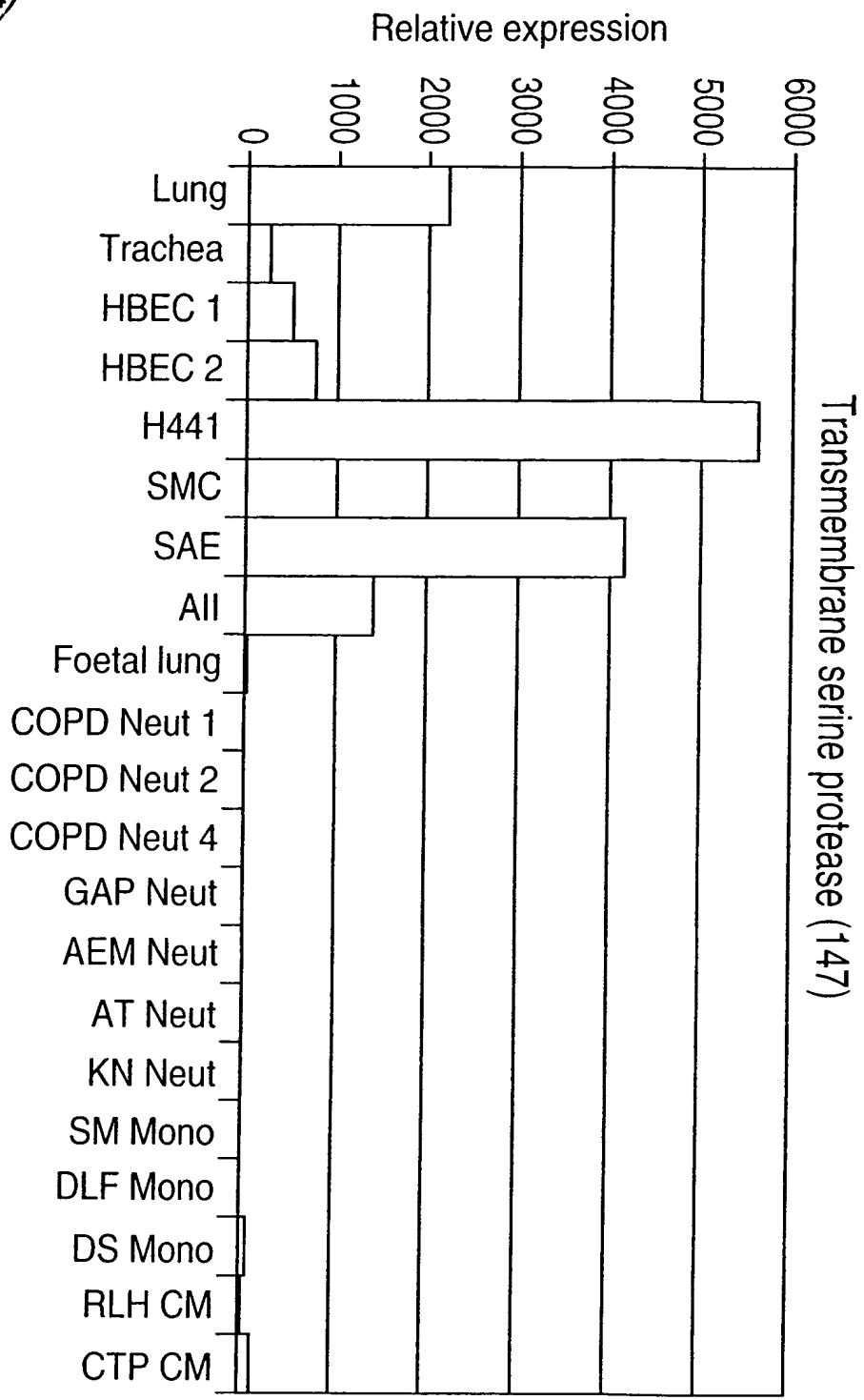


FIG. 4

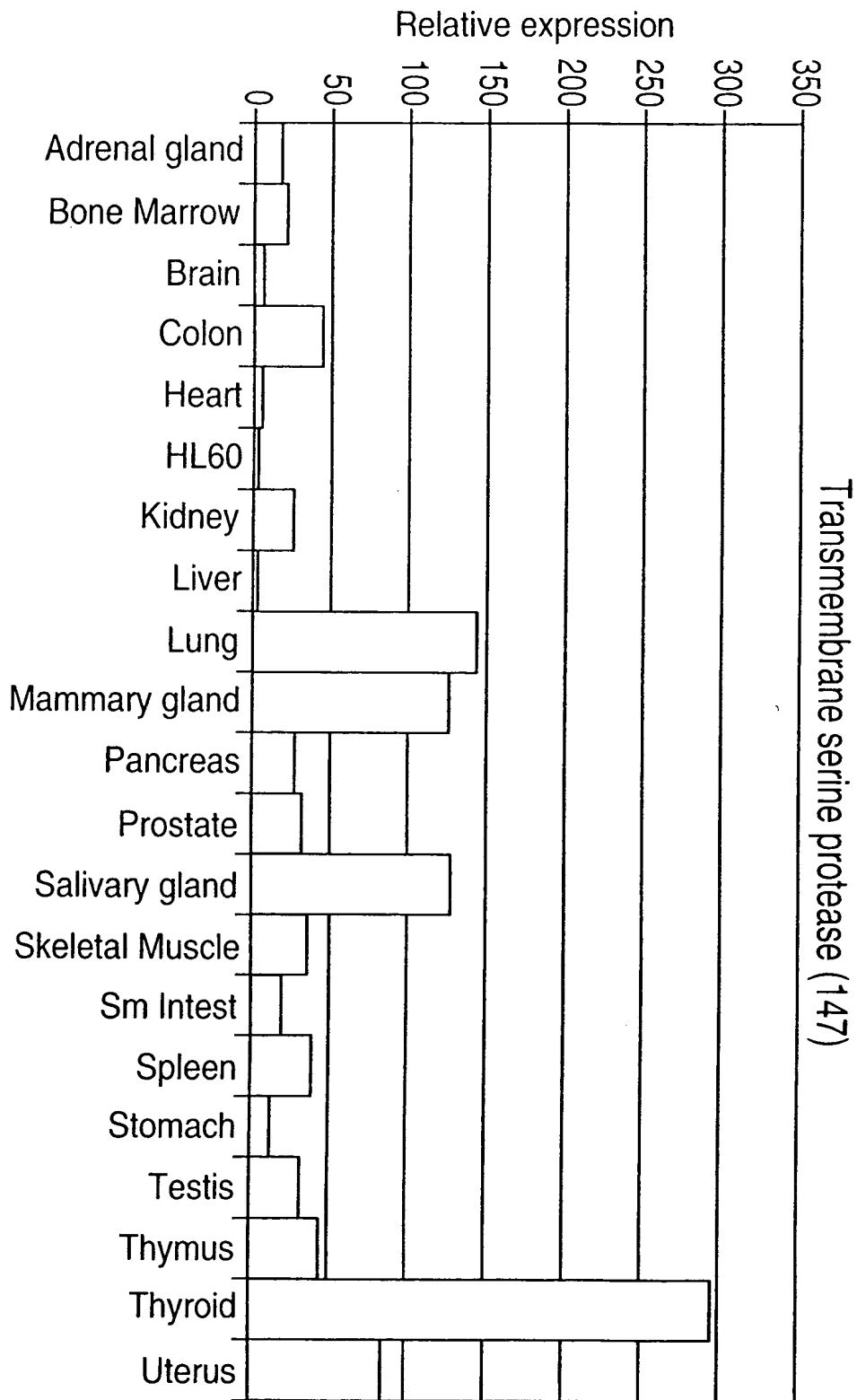
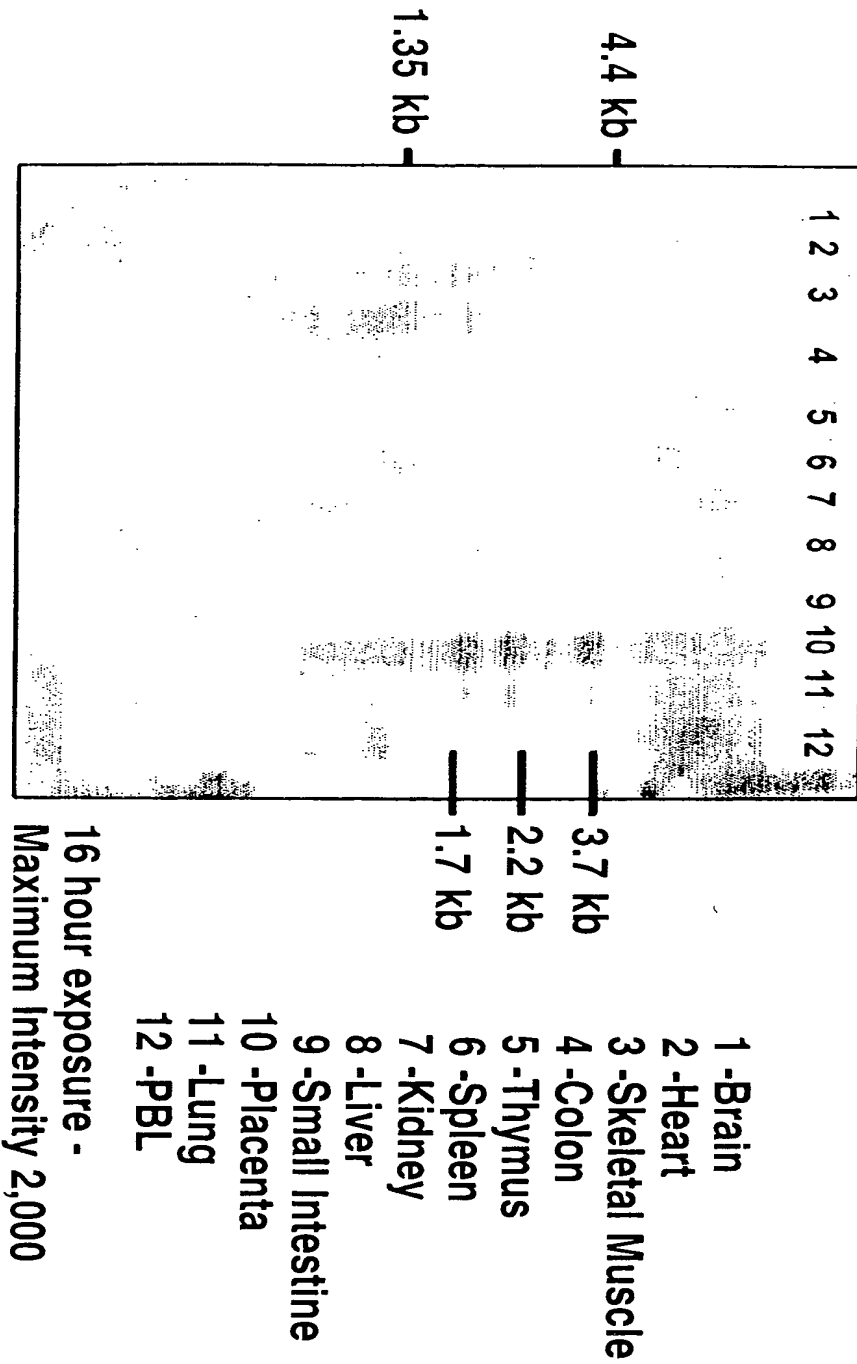


FIG. 5

FIG. 6

LBRI -147 - Transmembrane serine protease



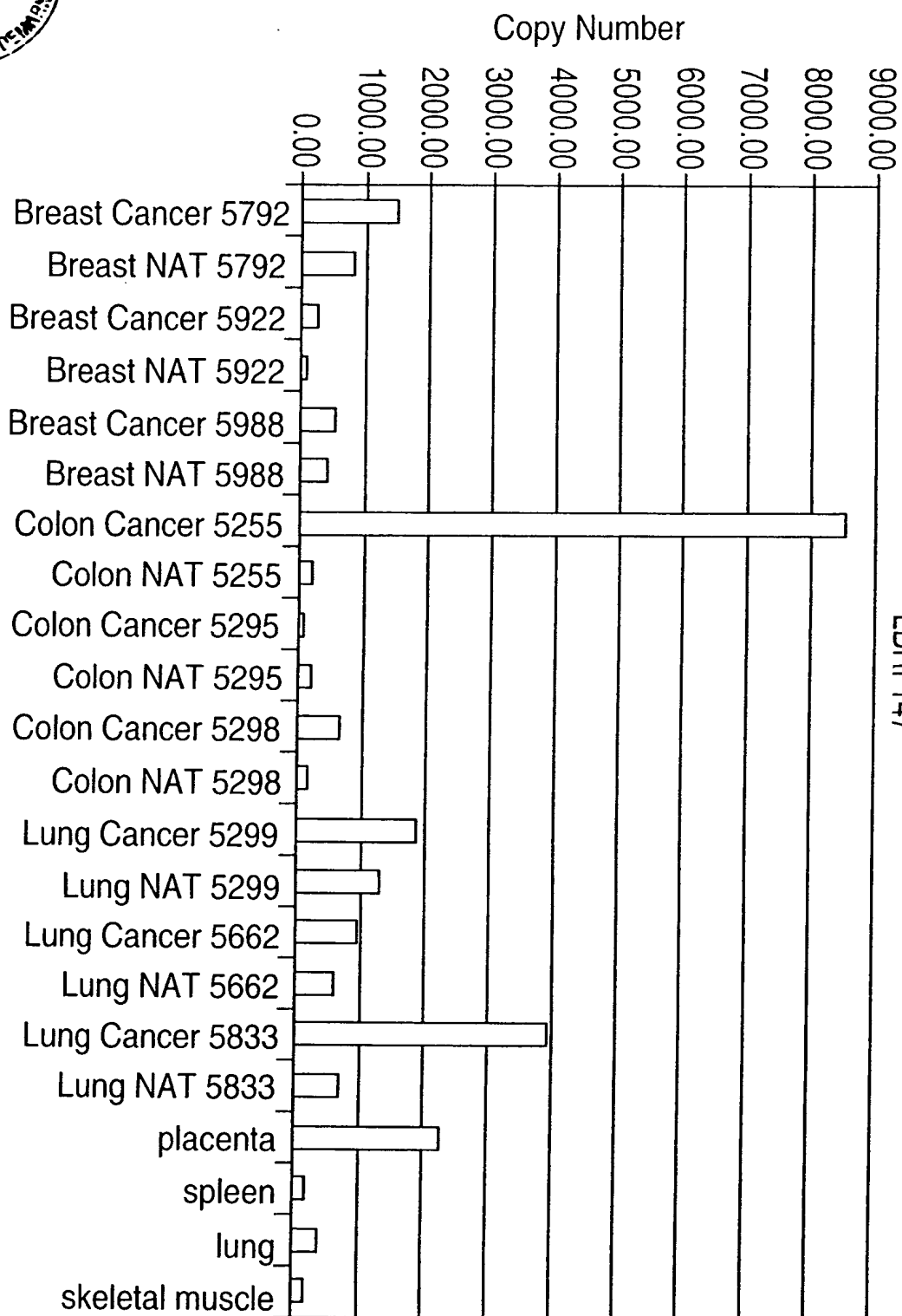


FIG. 7
LBRI 147



FIG. 8
LBRI 147: Fold Change

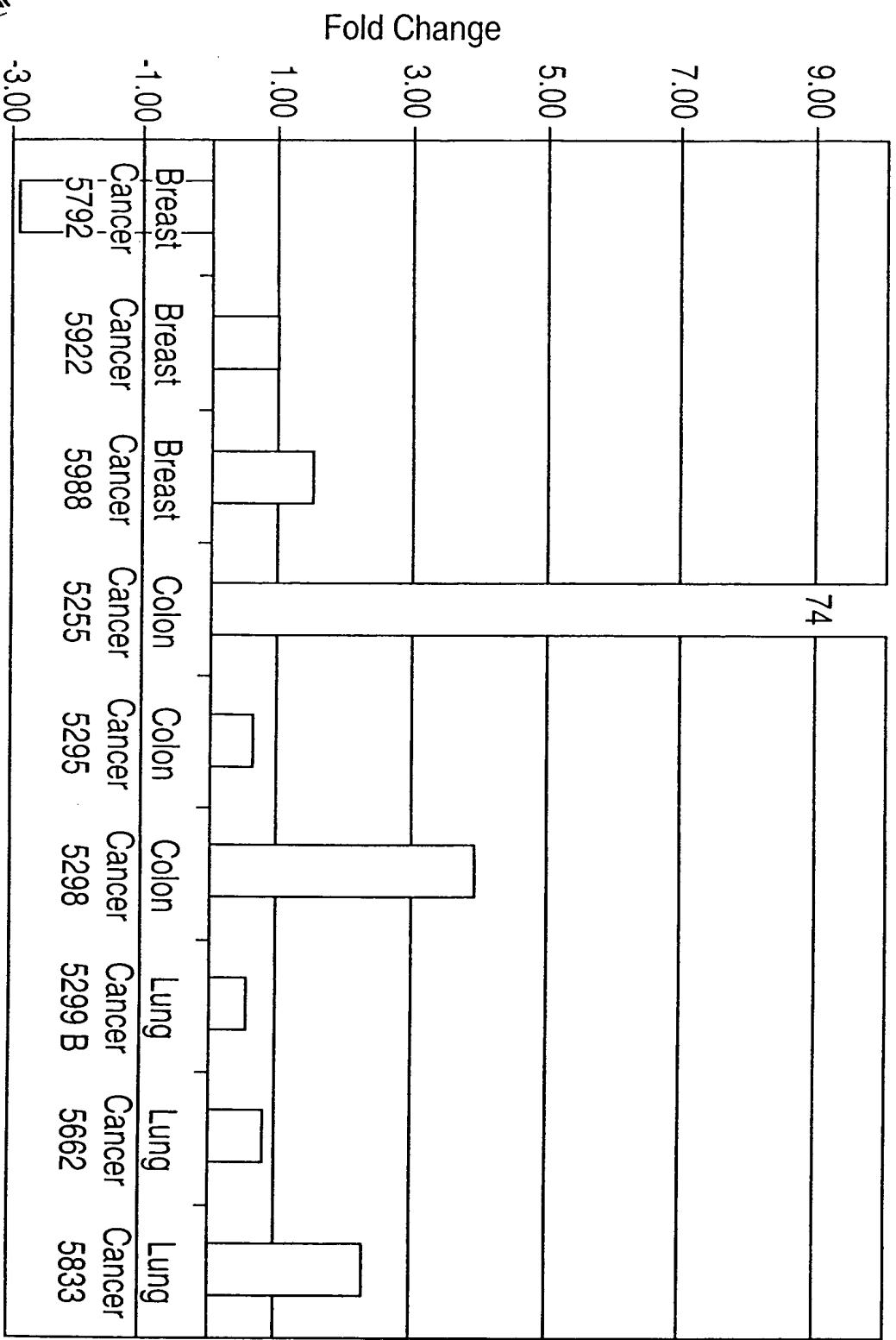


FIG. 8
LBRI 147: Fold Change

FIG. 9

